Amendments to the Specification

Please replace the paragraph beginning at page 6, lines 13-20, with the following amended paragraph:

The peptides listed in Table 1 are reported to be antagonists of the FP receptor that disrupt the interaction between the FP receptor and the associated $G_{\alpha q}$ protein (WO 99/32640 and WO ~~00/17438~~ 00/17348). The amino acids are indicated according to the standard IUPAC single letter convention, and X is cyclohexyl alanine. Lower case letters indicate L-amino acids and capital letters indicate D-amino acids. All of the disclosure in WO 99/32640 and WO ~~00/17438~~ 00/17348 relating to specific peptides as FP receptor antagonists, is hereby incorporated herein by reference.

Please replace Table 1 beginning on page 6, line 21, with the following amended Table 1.

Table 1

PCP-1	rvkfksqqhrqgrshhlem (SEQ ID NO:1)
PCP-2	rkavlknlyklasqccgvhvislhiwelssiknslkvaaisespvaeksast (SEQ ID NO:2)
PCP-3	clseeakearrindeierqlrrdkrdarre-NH_2 (SEQ ID NO:3)
PCP-4	kdtilqlnlkeynlv-NH_2 (SEQ ID NO:4)
PCP-8	ilghrdyk (SEQ ID NO:5)
PCP-10	wedrfyll (SEQ ID NO:6)
PCP-13	ILGHRDYK
PCP-14	YQDRFYLL
PCP-13.7	ILAHRDYK
PCP-13.8	ILaHRDYK
PCP-13.11	ILGFRDYK
PCP-13.13	ILGHKDYK
PCP-13.14	ILGHRNYK
PCP-13.18	ILGHQDYK
PCP-13.20	ILGHRDY-amide
PCP-13.21	ILGHRDYK-amide
PCP-13.22	ILGWRDYK
PCP-13.24	ILGXRDYK
PCP-15	SNVLCSIF

Please replace the paragraph beginning at page 12, line 8, with the following amended paragraph:

Peptides described in WO 01/42281 (Hopital Sainte-Justine) eg: IFTSYLECL (SEQ ID NO:7), IFASYECL (SEQ ID NO:8), IFTSAECL (SEQ ID NO:9), IFTSYEAL (SEQ ID NO:10), ILASYECL (SEQ ID NO:11), IFTSTDCL (SEQ ID NO:12), ~~TSYEAL~~ XTSYEAL (~~with~~ where X is 4-biphenyl alanine) (SEQ ID NO:13), ~~TSYEAL~~ XTSYEAL (~~with~~ where X is homophenyl alanine) (SEQ ID NO:14) are also described as EP4 receptor antagonists, as are some of the compounds described in WO 00/18744 (Fujisawa Pharm Co Ltd). The 5-thia-prostaglandin E derivatives described in WO 00/03980 (EP 1 097 922) (Ono Pharm Co Ltd) may be EP4 receptor antagonists.

Please replace the paragraph beginning at page 28, line 1, with the following amended paragraph:

To measure cDNA expression a reaction mix was prepared containing Taqman buffer (5.5 mM $MgCl_2$, 200 μM dATP, 200 μM dCTP, 200 μM dGTP, 400 μM dUTP), ribosomal 18S forward and reverse primers and probe (all at 50 nM), forward and reverse primers for EP receptor (300 nM), EP receptor probe (100 nM), AmpErase UNG (0.01 U/μl) and AmpliTaq Gold DNA Polymerase (0.025 U/μl; all from PE Biosystems). After mixing, 48 μl was aliquoted into separate tubes and 2 μl/replicate (40 ng) of cDNA added and mixed before placing duplicate 24 μl samples into a PCR plate. A no template control (containing water) was included in triplicate. Wells were sealed with optical caps and the PCR reaction carried out using an ABI Prism 7700. FP receptor primers and probe for quantitative PCR were designed using the PRIMER express program (PE Biosystems). The sequence of the FP receptor primers and probe were; Forward 5'-GCA GCT GCG CTT CTT TCA A-3' (SEQ ID NO: 15); Reverse 5'–CAC TGT CAT GAA GAT TAC TGA AAA AAA TAC-3' (SEQ ID NO: 16); Probe (FAM labelled) 5'–CAC AAC CTG CCA GAC GGA AAA CCG-3' (SEQ ID NO: 17).

Please replace the paragraph beginning at page 28, line 16, with the following amended paragraph:

The ribosomal 18S primers and probe sequences were; Forward 5' –CGG CTA CCA CAT CCA AGG AA-3' (SEQ ID NO:18); Reverse 5'–GCT GGA ATT ACC GCG GCT-3' (SEQ ID NO: 19); Probe (VIC labelled) 5'–TGC TGG CAC CAG ACT TGC CCT C-3' (SEQ ID NO: 20). Data were analysed and processed using Sequence Detector v1.6.3 (PE Biosystems) as instructed by the manufacturer. Briefly, the software calculates the reaction cycle number at which fluorescence reaches a determined level for both 18S control and FP receptor. This is the relative abundance of FP receptor in each sample and by comparing to an internal positive control, relative expression can be determined. Results are expressed as relative expression to the internal positive standard.